**In the Claims:**

Please cancel without prejudice all claims now pending. This includes claims 1-7, 9 and 17.

Please add new claims 20-45 as follows:

-- 20. An isolated polynucleotide encoding a protein with an amino acid sequence comprising the sequence of SEQ ID NO:2 and wherein said polynucleotide may be used to recombinantly engineer bacteria with an enhanced ability to produce amino acids by fermentation.

21. An isolated polynucleotide consisting essentially of nucleotides 252 – 1673 of SEQ ID NO:1 and degenerate variants thereof.

22. An isolated polynucleotide consisting of nucleotides encoding a protein consisting essentially of the amino acid sequence of SEQ ID NO:2.

B2

23. The isolated polynucleotide of claim 20 wherein said amino acid sequence is, at a minimum, 70% identical to that of SEQ ID NO:2.

24. The isolated polynucleotide of claim 20, wherein said amino acid sequence is, at a minimum, 80% identical to SEQ ID NO:2.

25. The isolated polynucleotide of claim 20, wherein said amino acid sequence is, at a minimum, 90% identical to SEQ. ID NO:2.

26. The isolated polynucleotide of claim 20, wherein said amino acid sequence is, at a minimum, 95% identical to SEQ ID NO:2.

27. An isolated polynucleotide comprising the nucleotide sequence of SEQ ID NO:1 or its complement.

28. The isolated polynucleotide of claim 27, wherein said nucleotide sequence is, at a minimum, at least 70% identical to that of SEQ ID NO:1.

29. The isolated polynucleotide of claim 27, wherein said nucleotide sequence is, at a minimum, at least 80% identical to that of SEQ ID NO:1.

30. The isolated polynucleotide of claim 27, wherein said nucleotide sequence is, at a minimum, at least 90% identical to that of SEQ ID NO:1.

31. The isolated polynucleotide of claim 27, wherein said nucleotide sequence is, at a minimum, at least 95% identical to that of SEQ ID NO:1.

32. A vector comprising a sequence identical to that of the isolated polynucleotide of any one of claims 20-31.

B2 cont.

33. A bacterium transformed with the vector of claim 32.

34. The bacterium of claim 33, wherein said vector is integrated into the bacterial genome and disrupts the endogenous mikE17 gene.

35. The vector pCR2.1mikE17int.

36. A bacterium transformed with the vector of claim 35.

37. A bacterium comprising an endogenous mikE17 gene that has been attenuated.

38. The bacterium of claim 37, wherein said mikE17 gene has been disrupted due to the integration of a vector, wherein said vector comprises a sequence of at least 15 successive nucleotides identical to 15 successive nucleotides in SEQ ID NO:1.

39. The isolated polynucleotide of any one of claims 20, or 24-26, wherein said polynucleotide is isolated from a coryneform bacterium

40. An isolated polynucleotide which hybridizes under stringent conditions to the complement of SEQ ID NO:1 wherein said stringent conditions comprise washing in 0.5X SSC at a temperature of 50 to 68 °C.

41. An isolated polynucleotide which hybridizes under stringent conditions to the complement of SEQ ID NO:1 wherein said stringent conditions comprise washing in 0.1X SSC at a temperature of 50 to 68 °C.

B2 cont.

42. The isolated polynucleotide of either claim 40 or 41, wherein said polynucleotide encodes a protein consisting essentially of the amino acid sequence of SEQ ID NO:2.

43. The isolated polynucleotide of any one of claims 40-42, wherein said polynucleotide is isolated from a coryneform bacterium.

44. An isolated polynucleotide consisting essentially of at least 30 consecutive nucleotides from the complement of SEQ ID NO:1 having the function of a probe in a hybridization reaction that may be used to isolate or identify a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:2.

45. A vector comprising the polynucleotide of claim 44. --